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Title:
Perfect score:
Sequence:
Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                    Run on:
                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
                                              irched:
                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                         US-09-836-077-3
3615
1 MTPPPPGRAAPSAPRARÝPG.....LAASLWLGVLPTLTLGLLVH 666
                                                                                                                                                                                                                        March 14, 2003, 09:23:54; Search time 19.4774 Seconds (without alignments) 3287.177 Million cell updates/sec
                                        283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
      283224
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	o	5	4	ω	2	_	No.	Result
139	170	174	186	190	215	228	236.5	312	363	364	399	407	408.5	409	411	452	479.5	485.5	597.5	611	612	617	617	621	628.5	632.5	654.5	1353	Score	
3.8	4.7	4.8	5.1	5. ω	5.9	6.3	6.5	8.6	10.0	10.1	11.0	11.3	11.3	11:3	11.4	12.5	13.3	13.4	16.5	16.9	16.9	17.1	17.1	17.2	17.4	17.5	18.1	37.4	Match	Query
1375	1884	1872	1905	1945	1894	295	2051	676	403	441	656	724	711	1074	712	730	834	760	751	753	666	782	749	772	748	772	771	653	Match Length DB	
1 JC5148	2 JC4975	2 JC4976	2 151553	2 T13937	2 JC4980	2 JQ17	2 T13164	2 T33853	2 E425	2 S29921	2 B49423	2 C49423	2 A49423	2 JC5928	2 T27165	2 ЈН0798	2 \$66498	2 148745	2 148748	2 G021	2 158169	2 148746	2 G01856	2 1487	2 148744	2 A49069	2 D49423	2 T03102	DB ID	
48	975	176	553	37	086	75	164	353	521)21	23	123	123	28	65	198	861	145	748	L 7 3	69	146	356	147	144)69	123	02		
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nepatocyte growth	2 prec	3 preci	- Afri	A - fruit	1 precursor	alL9R protein -	lexin B - fruit			•	orin I	ΙI	н		etical	fasciclin IV precu	M-sema F protein p	orin B -	orin E	orin II	orin II	orin C	orin V	orin D	orin A -				ption	
owth	precursor	precursor	African c	uit f	ursor	- v	uit f	prote	- vac	prote	- fru	prec	precu	precu	prote	precu	ein p	- mou	mou	I fam	ı m	- mou	- hum	- mou	mou	chicke	III pre	homolog	1 1 1	
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microcystin synthe	supervillin P205 -	hepatocyte growth polyprotein - pars	14R protein - vari	A43R protein - var	A46R protein - var	multidrug resistan	DNA-directed DNA p	osteonidogen - hum	SalflR protein - v	protein-tyrosine k	hypothetical prote	semaphorin recepto	hepatocyte growth

ALIGNMENTS

T03102	
semaphorin	in homolog A3 - alcelaphine herpesvirus 1
C; Date:	c;betcies: alceraphilie herpesvirus i C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
R; Ensser	T VINCT 71 CE17 CEC 1007
J. Virol. A;Title: A;Referen	J. Viroi. 71, 6517-6525, 1997 A;Title: Primary structure of the alcelaphine herpesvirus 1 genome. A;Reference number: 214840; MUJD:97404659; PMID:9261371
A; Access A; Status	A;Accession: T03102 A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecu A; Residu	
A; Cross-	A;Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58054.1; PID:g2337970
Query	Match 37.4%; Score 1353; DB 2; Length 653;
Matche	Matches 277; Conservative 86; Mismatches 228; Indels 12; Gaps 7;
Оу 22	2 PARLG-LPLRLELLLIMAAAASAQGHLRSGPRIFAVWKGHVGQDRVDFGQTEPHTVLFH 80
Db 45	5 PAAMGTLCVSIRLLMIL-SAITAAKSRFIDKPRLIVNLTDGFGQHRF-FGPQEPHTVLFH 102
Qу 81	
Db 103	3 SLNSSDVYVGGNNTIYLFDFAHSSNASTALINITSTHNTHRLSSTCENFITLLHNQTDGL 162
Оу 141	LACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDEN
Db 163	3 LACGTNSOKPSCWLINNLTTQFLGPKLGLAPFSPSSGNLVLFDQNDTYSTINLYKSLSGS 222
Qy 201	PRFRRIRGESELYTSDTVMQ
Db 223	3 HKFRRIAGQVELYTSDTAMHRPQFVQATAVHKNESYDDKIYFFFQENSHSDFKQFFHTVP 282
Оу 261	1 RVAQLCRCDQGGESSLSVSKWNTFLKAMLVCSDAATNKNENRLQDVFLLPDPSGQWRDTR 320
Db 283	
. Оу 321	
Db 343	3 IYGLFLSPWNFSAVCVFTVKDIDHVFKTSKLKNYHHKLPTPRPGQCMKNHQHVPTETFQV 402
Qу 381	
Db 403	3 ADRYPEVADPVYQKNNAMEPIIQSKYIYTKLLVYRVEYGGVFWATIFYLTTIKGTIHI 460
Qy 439	9 VYEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGG 498
Db 461	

588

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A; Gene: GDB:SEMA1
A; Cross-references: GDB:283448
C; Superfamilv common
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Best Local S
Matches 194
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                                                            446
                                                                                                 413
                       469 WYDLEEVLLEEMTVFREPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECC
                                                                                                                                                                              353
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                                                                                                                                                                                                                                                                                                                                               235 AYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                               VEPMG----PLKTPLFHSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVE-PGEQ
                                                                                                                                                                          LGPYAHRDGPNYQWVPYQGRVPYPRPGTCPSKTFGGFDSTKDLPDDVITFARSHPAMYNP
                                                                                              VEPMNNRPIVIKTDV---NYQETQIVVDRVDAEDGQ-YDVMFIGTDVGTVLKVVSIPKET
                                                          EHSFAFNIM-EIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCL
                                                                                                                                                                                                                                                  GPNGIDTHFDELQDVFLMNFKDP----KNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVF
                                                                                                                                                                                                                                                                          ATN---KNFNRLQDVFLL--PDPSGQWRDTRVYGVF---SNPWNYSAVCVYSLGDIDKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                       LVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQNPQFIKATIVHQ-DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNQTHLYACGTGAFHPIC-----TYIEIGHHPEDNIFKLENSHFENGRGKSPYDPKLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSE-GLLACGTNARHPSCWNLVNGTVVPLGEM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTK------GSCLDKRDCENYITLLER 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIVCLFWGVLLTARANYQNGKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DCFSCFMSRDPLCTWYNNTC---SFKQRVSVETGGPANRTLSEMCGDHYAPTVVKHQVSI
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                                                                                                                                                                                                             -RTSSLKGYHSSLPNPRPGKC-----LPDQQPIPTETFQVADRHPEVAQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.1%; Score 654.5; DB 2; 28.2%; Pred. No. 6.9e-42; tive 115; Mismatches 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAA65938.1;
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A;Residues: 1-772 <LUO>
A;Cross-references: GB:U02528; NID:g410078; PIDN:AAC59638.1; PID:g410079
C;Superfamily: semaphorin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Luo, Y.; Raible, D.; Raper, J.A. Cell 75, 217-227, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collapsin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999
C;Accession: A49069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                SHPAMYNPVFPINSRPIMIKTDV---DYQFTQIVVDRVDAEDGQ-YDVMFIGTDIGTVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PESPDENSLYLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQNPQFIKA 227
GKACAECCLARDPYCAWDGSSCSRYFPTAKRRTRRQDIRNGDPLTHCSDLQHHDNPSGQT
                                     GGGCHGCLMSRDPYCGWDQGRCISIY -- SSERSVLQSINPAEPHKEC -- -- -- PNPKPDK
                                                                                                                                                                                                                                                                    LGDIDKVF----
                                                                                                                                                                                                                                                                                                       ARLICSVPGPNGIDTHFDELQDVFLMNSKDP----KNPIVYGVFTTSSNIFKGSAVCMYS
                                                                                                                                                                                                                                                                                                                                                                                HLIPESDNPEDDKIYFFFRENAIDGEHTGKATHARIGQICKNDFGGHRSL-VNKWTTFLK
                                                                                                                                                                                                                                                                                                                                                                                                   NFIKVLKTYNQTHLYACGTGAFHPMC----TYIEVGSHPEDNIFRMEDSHFENGRGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYITLLERRSE-GLLACGTNARHPSCWNLVNGTVVPLGEM-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSRLYVGAKDHIFSFNL------VNIKEYQKIVWPVSHSRRDECKWAGKDILRECA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IALLSLGVLLAGRVNCQHVKNNVPRLKLSYKEMLESNNIVNFNGLANSSSYHTFLLDEE- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAVEHGFIQTLLKVTL---EVIDTEHL 673
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                                                                          VVSIPKETWHELEEVLLEEMTVFREPTVISAMKISTKQQQLYIGSATGVSQLPLHRCDVY
                                                                                                           VVE-PGEQEHSFAFNIM-EIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVY
                                                                                                                                                                                        RHPEVAQRVEPMGP----LKTPLFHSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHK 438
                                                                                                                                                                                                                               MTDVRRVFLGPYAHRDGPNYQWVPYQGRVPYPRPGTCPSKTFGGFDSTKDLPDEVITFAR
                                                                                                                                                                                                                                                                                                                                           AMLVCSDAATN---KNFNRLQDVFLL--PDPSGQWRDTRVYGVF---SNPWNYSAVCVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYDPKLLTASLLVDGELYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPRFISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSVWVGGRGKVYLFDFPEGKNASVRTVNI-----GSTKGSCL-----DKRDCE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEAQEGSYFREAQHWQLLPEDGIMAEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCI----LFIENLTAQQYGHYF 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LARDPYCAWDGSACSRYFPTAKRRTRRQDIRNGDPLTHCSDLHHDNHHGHSPEERIIYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENSSTFLECSPKSQRALVYWQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQQKDSGNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            llarity 28.4%; Pred. No. 3.3e-40; Conservative 101; Mismatches 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.5%; Score 632.5; 28.4%; Pred. No. 3.
                                                                                                                                                                                                                                                                -RTSSLKGYHSSLPNPRPGKC-----LPDQQPIPTETFQVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640
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772;

and

paralysis

of

125;

28;

----RGYA 170

169

580

496

460

404 382 344 338

288 286 229

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semaphorin A - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I48744
Puschel, A.W.; Adams, R.H.; Betz, H.
ron 14, 941-948, 1995
A;Reference number: I48744; MUID:95267431; pMID:7748561
A;Reference number: I48744; MUID:95267431; pMID:7748561
A;Accession: I48744
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-748 <RES>
A;Cross-references: EMBL:X85990; NID:g854323; PIDN:CAA59982.1; PID:g854324
C:Gene: semA
C;Superfamily: semaphorin
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Matches 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILFIENLTAQQYGHYFCEAQEGSYFR
| : : | : | | | | | : :
-LLLRSLQRRDSGIYFCHAVEHGFIQ
                                                                                                                                                                                                                      GRRPNSEGLLLEELQVFEDSAAITSMQISSKRQQLYVASRAAVAQIALHRCTALGRACAE
                                                                                                                                                                                                                                              GEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHG
                                                                                                                                                                                                                                                                                                                                                                             RAFLGPLPHKEGPTHQWVSYQGRVPYPRPGMCPSKTFGTFSSTKDFPDDVIQFGRNHPLM
                                                                                                                                                                                                                                                                                                                                                                                                              KVF-----RTSSLKGYHSSLPNPRPGKC-----LPDQQPIPTETFQVADRHPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VCS--DAATIKNFURLQDVFLLPDPSGQWRDT-RVYGVFSUP---WNYSAVCVYSLGDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENPDDDKIYFFFRESAVEAAPAMGRMSVSRVGQICRNDLGGQRSL-VNKWTTFLKARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HQDQAYDDKIYYFFREDNPDKNPE-APLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHRPPSVLVGEELYSGVTADLMGRDFTIFRSLGQNPSLRTEPHDSRWLNEPKFVKVFWIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECMNFVRLLHAYNHTHLLACRTGAFHPTCALWRWATAGGTHASTGPEKLEDGKGKTPYDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APLQKVSLAPNSRYYLSCPMESRHATYSWR------HKENVEQS-----CEPGHQSPNC
                                 QYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHL
                                                                                                                                                                                 CLMSRDPYCGWDQGRCISIY--SSERSVLQSINPAEPHKECPNPKPDKAPLQKVSLAPNS
                                                                                                                                                                                                                                                                                                  YNPVLPMG--GRPLFLQVGAGYTFTQIAADRVAAADGH-YDVLFIGTDVGTVLKVISVPK
                                                                                                                                                                                                                                                                                                                                    AQRVEPMGPLKTPLF---HSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKV--VEP 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCSVPGVEGDTHFDQLQDVFLL---SSRDRQTPLLYAVFSTSSGVFQGSAVCVYSMNDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DENSLYLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT - - - SDTVMQNPQFIKA-TIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEEKIIYGVENSSTFLECSPKSQRAIVYWQFQKQNDDHKVEIKVDDRMIRTEQG---
DSGVYLCVAVEQGFSQPLRRLVLHVLSAAQAERL
                                                                        GSAFLECEPRSLQAHVQWTFQGAGEAAHTQVLAEERVERTARG
                                                                                                                                              CCLARDPYCAWDGSACTREQPTAKRRERRQDIRNGDPSTLCSGDSSHSVLLEKKVLGVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.4%; Score 628.5; DB 2 31.5%; Pred. No. 6.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76; Mismatches 244;
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                                                                                                           -KENVEQSCEPGHQSPNCILFIENLTAQ 606
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semaphorin D - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: 148747
R;Puschel, A.W.; Adams, R.H.; Betz, H.
Reuron 14, 941-948, 1995
A;Reference number: 148744; MUID:95267431; PMID:7748561
A;Accession: 148747
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C;Superfamily:
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-772 < RES>
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I48747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLLACGTNARHPSCWNLVNGTVVPLGEM------
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                                                                                                                                                                                                                                                                                                 G----PLKTPLFHSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVE-PGEQEHSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLYACGTGAFHPIC-----TYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLL 181
CHAVEHGFMQTLLKVTL - - - EVIDTEHL
                                CEAQEGSYFREAQHWQLLPEDGIMAEHL 640
                                                                                                                                                                        PYCGWDQGRCISIY -- SSERSVLQSINPAEPHKECPN-----PKPDKAPLQKVSLA
                                                                                                                                                                                                                              AFNIM-EIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRD
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                                                                                                                                                                                                                                                                             NNRPIMIKTDV---NYQFTQIVVDRVDAEDGQ-YDVMFIGTDVGTVLKVVSVPKETWHDL 472
                                                                                                                                                                                                                                                                                                                                                  AHRDGPNYQWVPYQGRVPYPRPGTCPSKTFGGFDSTKDLPDDVITFGRSHPAMYNPVFPI
                                                                                                                                                                                                                                                                                                                                                                                ----RTSSLKGYHSSLPNPRPGKC-----LPDQQPIPTETFQVADRHPEVAQRVEPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     --KNFNRLQDVFLL--PDPSGQWRDTRVYGVF---SNPWNYSAVCVYSLGDIDKVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVYFFFRENAIGGEHSGKATHARIGQICKNDFGGHRSL-VNKWTTFLKARLICSVPGPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDGELYSGTAADFMGRDFAIFRTLGDHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQNPQFIKATIV-HQDQAYDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWVGGRGKVYLFDFPEGKNASVRTVNIGSTK-----GSCLDKRDCENYITLLERRSE- 138
                                                                                                     PNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCI-----LFIENLTAQQYGHYF
                                                                                                                                       PYCAWDGSSCSRYFPTAKRRTRRQDIRNGDPLTHCSDLEDHDNHHGPSLEERIIYGVE--
                                                                                                                                                                                                          EEVLLEEMTVFREPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARD
                                                                  -NSSTFLECSPKSQRALVYWQFQRRNRRSKREIRMGDHIIRTEQGLLLRSLQKKDSGNYL
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Similarity 27.5%;
89; Conservative 11
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.5e-39;
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C;Species:
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A;Residues: 1-749 <SEK>
A;Cross references: EMBL:U28369; NID:g974283; PIDN:AAD09138.1;
C;Superfamily: semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        semaphorin V - human
c; Species: Homo sapiens (man)
C; Date: 21-Dec-1996 #sequence
C; Accession: G01856
R; Sekido, Y.
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G01856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: G01856
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                                                                                                                                                                                                                                                                                        H-YDVLFIGTDVGTVLKVISVPKGSRPSAEGLLLEELHVFEDSAAVTSMQISSKRHQLYV
                                                                                                                                                                                                                                                                                                                        ETFHVLYLTTDRGTIHKV--VEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYV 479
                                                                                                                            EQSCEPGHQSPNCILFIENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHL
                                                                                                                                                            STLCSGDSSRPALLEHKVFGVEGSSAFLECEPRSLQARVEWTFQRAGVTAHTQVLAEERT 622
                                                                                                                                                                                            HKECPNPKPDKAPLQ-KVSLAPNSRYYLSCPMESRHATYSWRH------KENV 583
                                                                                                                                                                                                                          ASRSAVAQIALHRCAAHGRVCTECCLARDPYCAWDGVACTRFQPSAKRRFRRQDVRNGDP
                                                                                                                                                                                                                                                          SSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSS--ERSVLQSINPAEP
                                                                                                                                                                                                                                                                                                                                                        GTFSSTKDFPDDVIQFARNHPLMYNSVLPTG--GRPLFLQVGANYTFTQIAADRVAAADG
                                                                                                                                                                                                                                                                                                                                                                                        --LPDQQPIPTETFQVADRHPEVAQRVEPMGPLKTPLF---HSKYHYQKVAVHRMQASHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFSNP---WNYSAVCVYSLGDIDKVF-----RTSSLKGYHSSLPNPRPGKC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRNDVGGQRSL-VNKWTTFLKARLVCSVPGVEGDTHFDQLQDVFLL--SSRDHRTPLLYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELYT---SDTVMQNPQFIKA-TIVHQDQAYDDKIYYFFREDNPDKNPE-APLNVSRVAQL
 Mus -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRAGAAAV---IPG------LALLWAVGLGSAAPSPPRLRLSFQELQAWH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRAAPSAPRARVPGPPARLGLPLRLLLLLWA----AAASAQGHLRSGPRIFAVWKGHV
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 mouse (fragment)
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(house mouse)
                                                                                              -LLLRRLRRDSGVYLCAAVEQGFTQPLRRLSLHVLSATQAERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -EMRGYAPESPDENSLYLFEGDEVYSTIRKQEYNGKIPRFRRIRGES
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28.2%;
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Pred. No. 4.9e-39;
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C;Superfamily: semaphorin
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C;Accession: I48746
R;Puschel, A.W.; Adams, I
Neuron 14, 941-948, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 193;
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GSQQGLGVFQCWSIEEGFQQLVASYCPEVMEEGVM
                                                               K-PCKQVQIQPNTVNTLACPLLSNLATRLWVH-----NGAPVNASASCRVLPTGDLLLV 590
                                                                                                                                                              CHGCLMSRDPYCGWDQGRC--ISIYS---SERSVLQSINPAEPHKECPNPK-----PD
                                                                                              KAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNC-ILFIENL---
                                                                                                                               CGDCLLARDPYCAWTGSACRLASLYQPDLASRPWTQDIEGASVKELCKNSSYKARFLVPG
                                                                                                                                                                                                VTLSSRVHI----IEELQIFPQGQPVQNLLLDSHGGLLYASSHSGVVQVPVANCSLY-PT
                                                                                                                                                                                                                                                                                              ----HPEVAORVEPMGPLKTPLFHSKYHYOKVAVHRMQASHGETFHVLYLTTDRGTIHKV
                                                                                                                                                                                                                                                                                                                                                                 IDKVF-----RTSSLKGYHSSLPNPRPGKCLPD--QQPIPTETFQVADR------
                                                                                                                                                                                                                                                                                                                                                                                                                               MLVCSDAATNKNFNRLQDVFLL-PDPSGQWRDTRVYGVFSNPWNY-----SAVCVYSLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDQAY----DDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCQNYIKILLPLNSSHLLTCGTAAFSPLCAYIHIASFTLAQDEAGNVI-LEDGKGHCPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCENYI-TLLERRSEGLLACGTNARHPSC-----WNLVN---GTVVPLGEMRGYAPFS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTALLLSQDGKTLYVGAREALFALNSNLSFLPGGEYQELLWSADADRKQQCSFKGKDPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTVLFHEPGSSSVWVGGRGKVYLFD-----FPEGKNASVRTVNIGSTKGSCL-----DKR 124
                              -TAQQYGHYFC-EAQEGSYFREAQHWQLLPEDGIM
                                                                                                                                                                                                                               VEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGG
                                                                                                                                                                                                                                                               HFLMDGQVRSRLLLLQP------RARYQRVAVHRVPGLH-STYDVLFLGTGDGRLHKA
                                                                                                                                                                                                                                                                                                                                 VQKAFDGLYKKVNRETQQWYTETHQVPTPRPGACITNSARERKINSSLQLPDRVLNFLKD
                                                                                                                                                                                                                                                                                                                                                                                                    QLLCSRPDDGFPFNVLQDVFTLNPNPQ-DWRKTLSIGVFTSQWHRGTTEGSAICVFTMND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESLGSPIGDDDKIYFFFSETGQEFEFFENTIVSRVARVCKGDEGGERVLQ-QRWTSFLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNFKSTALVVDGELY-TGTVSSFQGNDPAISRSQSSRPTKTESSLNWLQDPAFVASATSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTV--MQNPQFIKATIVH
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Pred.
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No. 5.
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.2e-39;
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   625
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cemaphorin III - mouse (fragment)
c;Species: Mus musculus (house mouse)
c;Date: 26-7ul-1996 #sequence_revision
C;Accession: I58169

RESULT I58169

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R; Messersmith, E.K.; Leonardo, Neuron 14, 949-959, 1995

A;Title:

Semaphorin

can

function

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selective

chemorepellent

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Goodman, pattern s

E.D.;

Shatz, C.J.;

Tessier-Lavigne, M.;

C.S.;

26-Jul-1996 #text_change

24-Sep-1999

Matches

192;

Conservative

116;

Mismatches

281;

Indels

124;

30;

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semaphorin III family homolog - human C:Species: Homo sapiens (man) C:Date: 21-Dec-1996 #sequence_revision 06 C:Accession: G02173 R:Naylor, S. submitted to the EMBL Data Library, Octob A:Reference number: G09275 A:Accession: G02173 A:Status: preliminary; translated from GB A:Molecule type: mRNA A:Residues: 1-753 <NAYY A:Cross-references: EMBL:U38276; NID:g106 C:Superfamily: semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: I58169; MUID:95267432; PMID:7748562
A;Accession: I58169
A;Botatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-666 <RES>
A;Cross-references: GB:L40484; NID:9703189; PIDN:AAA73934.1; PID:9703190
C;GenetLcs:
A;Gene: SemaIII
C;Superfamily: semaphorin
                                                                                                                                                                                                                                                            RESULT
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 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIKATIV-HQDQAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173;
                                                                                                                                                                                                                                                                                                                                                                                            HHDNHHGPSLEERIIYGVE---NSSTFLECSPKSQRALVYWQFQRRNEDRKEEIKMGDHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPLHRCDIYGKACAECCLARDPYCAWDGSSCSRYFPTAKRRTRRQDIRNGDPLTHCSDLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTDRGTTHKVVE-PGEQEHSFAFNIM-EIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDDVITFARSHPAMYNPVFPINNRPIMIKTDV---NYQFTQIVVDRVDAEDGQ-YDVMFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CMYSMSDVRRV-----LLGPYAHRDGPNYQWVPYQGRVPYPRPGTCPSKTFGGFDSTKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVYSLGDIDKVFRTSSLKG------YHSSLPNPRPGKC-----LPDQQPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGKSPYDPKLLTASLLIDGELYSGTAANFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPR
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                                                                                                                                                                                                                                                                                                                                                            I-----LFIENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHL
                                                                                                                                                                                                                                                                                                                                                                                                                         ----PKPDKAPLQKVSLAPNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNC
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                                                                EMBL: U38276; NID: g1061350; PIDN: AAB18276.1;
 16.9%;
26.9%;
                                                                                                                                                             Library, October
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Pred.
                                                                                                              from GB/EMBL/DDBC
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No. 1
1; DB 2;
. 1.4e-38;
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                                                                PID:g1061351
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A; Gene: semE
C; Superfamily:
                                                                                                                                    A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-751 <RES>
                                                                                                                                                                                             A; Reference number: A; Accession: I48748
                                                                                                                                                                                                               A; Title: Murine semaphorin D/collapsin is A; Reference number: I48744; MUID:95267431;
                                                                                                                                                                                                                                                                                                            C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                semaphorin
C;Species:
                                                                                                                                                                                                                                                                                                                                                                      RESULT
148748
                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                     R; Puschel, A.W.; Adams, Neuron 14, 941-948, 1995
                                                                                                                                                                                                                                                                                          C; Accession:
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                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNFNRLQDVFLLPDPSGQWRDTR----VYGVFSNP----WNYSAVCVYSLGDIDKVFR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS---DAATN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYSCTATENNFKHVVTRVQL-----HVLGRDAVHAA-----LFPPLSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMLEEVEVFKDPAPVKTMTISSKRQQLYVASAVGVTHLSLHRCQAYGAACADCCLARDPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPLKTPLF---HSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKV-VEPGEQEHSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKEGPNYQWMPFSGKMPYPRPGTCPGGTFTPSMKSTKDYPDEVINFMRSHPLMYQAVYPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFFFRERSAEA-PQSPAVYARIGRICLNDDGGHCCL-VNKWSTFLKARLVCSVPGEDGIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --QRRPLVVRTGAPYRLTTIAVDQVDSADGR-YEVLFLGTDRGTVQKVIVLPKDDQEMEE
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                                                                                                                                                                                                                                                                                                                                                    (H)
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                                                                                                                                                                                                                                                                                          148748
                                                          semaphorin
                                                                                                                                                                                                                                                                                                                                                    mouse
                                                                                                                  EMBL: X85994;
                                                                                                                                                                                                                                                                       R.H.; Betz, H
  16.5%;
                                                                                                                NID: g854331; PIDN: CAA59986.1;
Score 597.5; DB 2; Pred. No. 1.5e-37;
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C;Superfamil
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C;Speciles: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
ession: I48745
ession: I48745
Schel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
 밁
                                                                                                                                                                            A; Molecule type: mRNĀ
A; Residues: 1-760 <RES>
A; Cross-references: EMBL: X85991;
                                                                                                                                                                                                                                                                                                                                                                                              RESULT
148745
                                                                                                                                                                                                                                            A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and A;Reference number: I48744; MUID:95267431; PMID:7748561 A;Accession: I48745
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                                                                                                                              Superfamily: semaphorin
                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                             Status: preliminary; translated
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                                32
                                                                  Local Similarity
les 198; Conserv
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                            RLLLLLWAAAASAQGHLRSGPRIFAVWKGHVGQDR--VDF----GQTEPHTVLFHEPGSS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IATENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YNSISPIH--RRPLIVRIGTDYKYTKIAVDRVNAADGR-YHVLFLGTDRGTVQKVVVLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VENGPEAHKEGPNHQLISYQGRIPYPRPGTCPGGAFTPNMRTTKDFPDDVVTFIRNHPLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCI----LFIENLTAQQYGHYFC 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMSRDPYCGWDQGRCISIY--SSERSVLQSINPAEPHKECP--NPKPDKAPLQKVSL-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSVTDEDGPETHFDELEDVFLLETDNP--RTTLVYGIFTTSSSVFKGSAVCVYHLSDIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CS---DAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVF---SNPWNYSAVCVYSLGDIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DENSIVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQNPQFIKATIVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAQEGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNSTFLECAPKSPQASIKWLLQKDKDRRKE-GKLNERIIATSQGLLIRSVQDSDQGLYHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLARDPYCAWDGHSCSRFYPTGKRRSRRQDVRHGNPLTQCRGFNLKAYRNAAEIVQYGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSSASGELILEELEVFKNHVPITTMEISSKKQQLYVSSNEGVSQVSLHRCHIYGTACADC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGNFVRVIQTFNRTHLYVCGSGAFSPVCTYLNRGRRSEDQVFMIDSKCESGKGRCSFNP
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                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620
                                                              13.4%; Score 485.5; DB 2;
27.0%; Pred. No. 5.9e-29;
rative 105; Mismatches 287;
                                                                                                                                                                                NID: g854325; PIDN: CAA59983.1;
                                                                                                                                                                                                                                 from GB/EMBL/DDBJ
-KYHAGDGHRALSFFQQKGLRDFDTLLLSDDG-N 74
                                                                                              Length
                                                              Indels
                                                                                              760;
                                                              143;
                                                                                                                                                                              PID:g854326
                                                            Gaps
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RESULT 12
$56.498
M-sema F protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
C:Accession: $66498
R:Inagaki, S.; Furuyama, T.; Iwahashi, Y.
FEBS Lett. 370, 269-272, 1995
A:Title: Identification of a member of mouse semaphorin family.
A:Reference number: $66498; MUID:95385809; PMID:7656991
                                                                       C;Superfamily: semaphorin
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-834/Product: M-sema F protein #status predicted <
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A; Residues: 1-834 <INA>
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                                                                                                                                  A;Cross-references: EMBL:S79463; NID:g1110598; PIDN:AAB35184.1; PID:g1110599
                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                            A; Accession: S66498
 Matches
                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MESRHATYSWRH-KENVEQSCEPGHQSPNCILFIENLTAQQYGHYFCEAQEGSY-FREAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPLF-HSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQ 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLTLLLASPLGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HW-----QLLPE-DGIMAEHL-----LGHACALAA--SLW------LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLCSLLSGSTKPWKQDMERGNPEWVCTRGPMARSPRRQSPPQLIKEVLTVPNSILELRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSPDSEPVRNLQLAPAQGAVFAGFSGGIWRVPRANCSVY-ESCVDCVLARDPHCAWDPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWD-QG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPLLVKSGVEYTRLAVESARGLDGSSHVVMYLGTSTGPLHKAVVP---QDSSAYLVEEIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFLMDEH------VVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLPFNIIRHAVLLPADSPS--VSRIYAVFTSQWQVGGTRSSAVCAFSLTDIERVFKGKYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNY-----SAVCVYSLGDIDKVFR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQVVYFFFEETASEFDFFEELYISRVAQVCKNDVGGEKLLQ-KKWTTFLKAQLLCAQPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VDGMLYSG-TMNNFLGSEPILMRTLG-----SHPVLKTDIFLR--WLHADASFVAAIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVLVSYNATHLYACGTFAFSPACTFIELQDSLLLPILIDKVMDGKGQSPLTLFTSTQAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TLLERRSEGLLACGTNARHPSCW--NLVNGTVVPL----GEMRGYAPFSPDENSLVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCISIYS-SERSVLQSINPAEPHKECP----NPKPDKAP--LQKVSLAPNSRYYLSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLYVGARETVLALNIQNPGIPRLKNMIPWPASER-----KKTECAFKKKSNETQCFNFI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVWVGGRGKVYLFD-----FPEGKN-----ASVRTVNIGSTKGSCLDKR-----DCENYI 130
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TSSLKGYHSSLPNPRPGKCLPDQQPIPTETFQ----VADRHPEVAQRVEPMGPLK 398
 Conservative
                   13.3%;
25.6%;
   108;
Pred. No. 2e-
); Mismatches
               Score 479.5; DE Pred. No. 2e-28;
                                     DB 2;
307;
                                                                               <MAT>
 Indels
                                     Length
 113;
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Gaps
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LWAAAASAQGHLRSGPRIFAVWKGHVGQDRVDFGQTEPHTVLFHEPG--

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F;628-652/Domain: transmembrane F;653-730/Domain: intracellular F;44,71,163,267,360,539/Binding
                                                                                      C;Keywords: glycoprotein; transmembrane protein F;1-22/Domain: signal sequence #status predicted F;23-730/Product: fasciclin IV #status predicted F;23-627/Domain: extracellular #status predicted
                                                                                                                                                      A; Experimental source: embryo C; Comment: This protein plays a role in growth cone guidance
                                                                                                                                                                                                                                                                                                                                                             fasciclin IV precursor - American bird grasshopper
C:Species: Schistocerca americana (American bird grasshopper)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
JH0798
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                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-730 < KOL>
                                                                                                                                                                                                                                                         A; Reference number: JH0798; A; Accession: JH0798
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R; Kolodkin, A.; Mati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLAHAHWTFGSQDLPAEQPGSFLYDTGLQALVVMAAQSRHSGPYRC----YSEEQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHATYSWRHKENVEQSCEPG---HQSPNCILFIENLTAQQYGHYFCEAQEGSYFREAQHW
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                                                                                                                                                                                                                                                                                                                Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, 5, 1992
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A; Accession: TZ7165
A; Status: preliminary; translated from A; Molecule type: DNA
A; Residues: 1-712 < WILL>
A; Cross references: EMBL: AL032653; PII
A; Experimental source: clone Y54E5B
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C;Date: 15-Oc
C;Accession:
R;Lennard, N.
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                                                                                                                                                                            A;Gene: CESP:Y54E5B.1
A;Map position: 1
A;Introns: 36/1; 70/2
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                                 RILTLLLFNVVRSSEAITGGVVNLRPKQIINSVGIG----DR--FGGIGTSSDESDHFK
                                                                   RLRLLLLWAAAASAQG-----HLRSGPRIFAVWKGHVGQDRVDFG-----QTEPHTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTAVGSPDWSAGKRRFIQNISLGE-HKAC
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LFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGS-----
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                                                                                                                                                                              36/1; 70/2;
                                                                                                           Conservative
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                                                                                                                                                                              85/3; 194/2; 221/1; 253/3; 301/1; 352/3;
                                                                                                       11.4%; Score 411; DB 2; 26.7%; Pred. No. 2.7e-23; tive 80; Mismatches 197
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9; Mismatches
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cches 229;
                                                                                                                                                                                                                                                                                                                                                                                  1998
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                                                                                                                                                                                                                                                                          GSPDB:GN00019;
                                                                                                                                           Length 712;
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-TKGSCLD
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599/3;

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A;Title: Molecular cloning and mapping of human semaphorin F from A;Reference number: JC5928, MUID:98125554; PMID:9464278
A;Accession: JC5928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       semaphorin F precursor - human
C;Speciles: Homo sapiens (man)
C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Nov-2000
C;Accession: JC5928
밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1074 <SIM>
A; Residues: 1-1074 <SIM>
A; Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584
Perimental source: brain
mment: This protein disrupts normal brain development and leads to some of the feature.
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                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: semaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                ;971-993/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                 Superfamily: human semaphorin F; thrombospondin type 1 repeat homology;1-20/Domain: signal sequence #status predicted <SIG>;50-533/Domain: semaphorin #status predicted <SEM>;840-896/Domain: thrombospondin type 1 repeat homology <THR3>
                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                        Matches
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105 YSKGKSKEECQNYIRVLLVGGDRLFTCGTNAFTPVCTNRSLSNLAEIHDQISGMARCPYS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375
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                                                                                                                                                                                      Local Similarity
nes 147; Conserv
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                                                                                                                                     64 QDRVDFGQTEPHTVLFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVN---IGSTKGSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
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                                           L----DKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPL-GEMRGYA--PFS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADEIASLPVHNC-AQQTSCSKCVQLQDPHCAWDSSIARCV 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQ--GRCI 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVYTVFSTPDSDVRMSAVCKFSMKKIREEFDNGTFKHQNNAQSMWMAFNRNEVPKPRPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VYGVFSNP---WNYSAVCVYSLGDIDKVFRTSSLKGYHSS------LPNPRPGK 365
                                                                                       KNAADFSQ-----LTFDPGQKELVVGARN--YLFRLQLEDLSLIQAVEWECDEATKKAC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNYDILFIGTSDGKVLKVVEVDGN----ATVIQSATVFQRGVPI--VNLLTTKESVVIVS 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSS 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARVCKNDKGGARPAN-ERWTSYLKARLNCSLPSGSSPFYFNELKAV---SDPIDAGNNNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIRGESELYTSDTVMQNPOFIKATIVHODOAYDDKIYYFFRE--DNPDKNPEAPLNVSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHNSSALYVPGTNQLFVATVTDFVGNDALIYRKTIDETPSSKSAANIRTQSYDAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DENSLVL----STIRKQEYNGKIPRFR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSPDSTKLPENTVSFILHHPLLHR----PIPSVAAPLLVEGADRADLTQITVLPRVRAVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQLCRGDQGGESSLSVSKWNTFLKAMLVCS--DAATNKNFNRLQDVFLLPDPSGQWRDTR
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                                                                                                                                                                                      Conservative
                                                                                                                                                                                                          11.3%; Score 409; DB 2
29.5%; Pred. No. 7e-23;
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                  DB 2; Length 1074;
                                                                                                                                                                                      Indels
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                                                                                                                                                                                      70;
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                                                                                                                                                                                    Gaps
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DPYCGWDVVMKKCTSLEES
                                                                                                                                                                                                                                                                                                                                                                                                                        TIVHQDQAYD--DKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFL
                                    DPYCGWD--QGRCISIYSS 524
                                                                                                                                                                                         -EPMGPLKT-PLF-HSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVEP-GEQEH 447
                                                                                                                                                                                                                                  IAQAF-SGPFKYQENSRSAWLPYPNPNPHFQCGTVDQGL---YVNLTERNLQDAQKFILV 382
                                                                                                                                                                                                                                                           IDKVFRTSSLKGYHSS-----LPNPRPG-KCLPDQQPIPTETFQVADRHPEVAQRV---
                                                                                                                                                                                                                                                                                                            KARLNCSRPGEVPFYYNELQSTFFLPELD-----LIYGIFTTNVNSIAASAVCVFNLSA 326
                                                                                                                                                                                                                                                                                                                                                  KAMLYCS-DAATNKNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWN---YSAVCVYSLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDENSLVLF-EGDEVYSTIRKQEYNGKIPRFRRIRG-----ESELYTSDTVMQNPQFIKA
                                                                         SCLLEEIELFPERRREPIRSLQILHSQSVLFVGLREHVVKIPLKRCQFYRTR-STCIGAQ
                                                                                                              SFAFNIMEIOPFRRAAAIOTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSR 507
                                                                                                                                                     HEVVQPVTTVPSFMEDNSRFSHVAVDVVQGREA-LVHIIYLATDYGTIKKVRVPLNQTSS
                                                                                                                                                                                                                                                                                                                                                                                         ----SSYDIGNFTYFFFRE-NAVEHDCGKTVFSRAARVCKNDIGGRFLLE-DTWTTFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQHNSTALLTAGGELYAA-TAMDFPGRDPAIYRSLGILPPLRTAQYNSKW-LNEPNFV--
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Search completed: March 14, 2003, 09:27:40 Job time : 24.4774 secs